

Figure 1

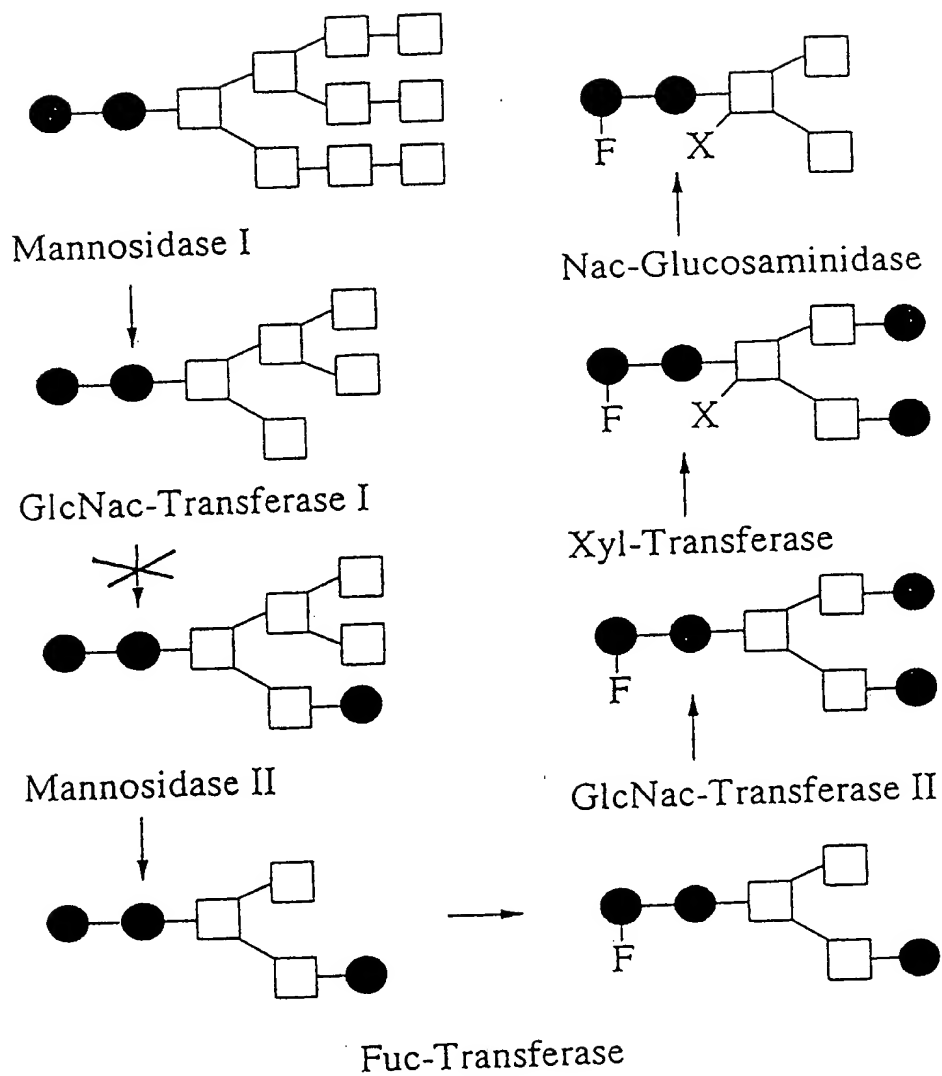


Figure 2

Al *GntI* cDNA

GAATTCGCGG CCGCCTGAGA AACCCCTCGAA TTCAATTTTCG CATTTGGCAG AG ATG 55  
Met  
1

AGA GGG AAC AAG TTT TGC TTT GAT TTA CGG TAC CTT CTC GTC GTG GCT 103  
Arg Gly Asn Lys Phe Cys Phe Asp Leu Arg Tyr Leu Leu Val Val Ala  
5 10 15

GCT CTC GCC TTC ATC TAC ATA CAG ATG CGG CTT TTC GCG ACA CAG TCA 151  
Ala Leu Ala Phe Ile Tyr Ile Gln Met Arg Leu Phe Ala Thr Gln Ser  
20 25 30

GAA TAT GTA GAC CGC CTT GCT GCT GCA ATT GAA GCA GAA AAT CAT TGT 199  
Glu Tyr Val Asp Arg Leu Ala Ala Ile Glu Ala Glu Asn His Cys  
35 40 45

ACA AGT CAG ACC AGA TTG CTT ATT GAC AAG ATT AGC CAG CAG CAA GGA 247  
Thr Ser Gln Thr Arg Leu Leu Ile Asp Lys Ile Ser Gln Gln Gln Gly  
50 55 60 65

AGA GTA GTA GCT CTT GAA GAA CAA ATG AAG CAT CAG GAC CAG GAG TGC 295  
Arg Val Val Ala Leu Glu Glu Gln Met Lys His Gln Asp Gln Glu Cys  
70 75 80

CGG CAA TTA AGG GCT CTT GTT CAG GAT CTT GAA AGT AAG GGC ATA AAA 343  
Arg Gln Leu Arg Ala Leu Val Gln Asp Leu Glu Ser Lys Gly Ile Lys  
85 90 95

AAG TTA ATC GGA GAT GTG CAG ATG CCA GTG GCA GCT GTA GTT GTT ATG 391  
Lys Leu Ile Gly Asp Val Gln Met Pro Val Ala Ala Val Val Val Met  
100 105 110

GCT TGC AGT CGT ACT GAC TAC CTG GAG AGG ACT ATT AAA TCC ATC TTA 439  
Ala Cys Ser Arg Thr Asp Tyr Leu Glu Arg Thr Ile Lys Ser Ile Leu  
115 120 125

AAA TAC CAA ACA TCT GTT GCA TCA AAA TAT CCT CTT TTC ATA TCC CAG 487  
Lys Tyr Gln Thr Ser Val Ala Ser Lys Tyr Pro Leu Phe Ile Ser Gln  
130 135 140 145

GAT GGA TCA AAT CCT GAT GTA AGA AAG CTT GCT TTG AGC TAT GGT CAG 535  
Asp Gly Ser Asn Pro Asp Val Arg Lys Leu Ala Leu Ser Tyr Gly Gln  
150 155 160

CTG ACG TAT ATG CAG CAC TTG GAT TAT GAA CCT GTG CAT ACT GAA AGA 583  
Leu Thr Tyr Met Gln His Leu Asp Tyr Glu Pro Val His Thr Glu Arg  
165 170 175

CCA GGG GAA CTG GTT GCA TAC TAC AAG ATT GCA CGT CAT TAC AAG TGG 631  
Pro Gly Glu Leu Val Ala Tyr Tyr Lys Ile Ala Arg His Tyr Lys Trp  
180 185 190

GCA TTG GAT CAG CTG TTT CAC AAG CAT AAT TTT AGC CGT GTT ATC ATA 679  
Ala Leu Asp Gln Leu Phe His Lys His Asn Phe Ser Arg Val Ile Ile  
195 200 205

CTA GAA GAT GAT ATG GAA ATT GCT GCT GAT TTT TTT GAC TAT TTT GAG 727  
Leu Glu Asp Asp Met Glu Ile Ala Ala Asp Phe Phe Asp Tyr Phe Glu  
210 215 220 225

Figure 2 (continued)

GCT GGA GCT ACT CTT CTT GAC AGA GAC AAG TCG ATT ATG GCT ATT TCT Ala Gly Ala Thr Leu Leu Asp Arg Asp Lys Ser Ile Met Ala Ile Ser 230 235 240	775
TCT TGG AAT GAC AAT GGA CAA AGG CAG TTC GTC CAA GAT CCT GAT GCT Ser Trp Asn Asp Asn Gly Gln Arg Gln Phe Val Gln Asp Pro Asp Ala 245 250 255	823
CTT TAC CGC TCA GAC TTT TTT CCT GGT CTT GGA TGG ATG CTT TCA AAA Leu Tyr Arg Ser Asp Phe Phe Pro Gly Leu Gly Trp Met Leu Ser Lys 260 265 270	871
TCA ACT TGG TCC GAA CTA TCT CCA AAG TGG CCA AAG GCT TAC TGG GAT Ser Thr Trp Ser Glu Leu Ser Pro Lys Trp Pro Lys Ala Tyr Trp Asp 275 280 285	919
GAC TGG CTA AGG CTG AAA GAA AAT CAC AGA GGT CGA CAA TTT ATT CGC Asp Trp Leu Arg Leu Lys Glu Asn His Arg Gly Arg Gln Phe Ile Arg 290 295 300 305	967
CCA GAA GTT TGC AGA ACG TAC AAT TTT GGT GAG CAT GGT TCT AGT TTG Pro Glu Val Cys Arg Thr Tyr Asn Phe Gly Glu His Gly Ser Ser Leu 310 315 320	1015
GGG CAG TTT TTT AAG CAG TAT CTT GAG CCA ATT AAG CTA AAT GAT GTC Gly Gln Phe Phe Lys Gln Tyr Leu Glu Pro Ile Lys Leu Asn Asp Val 325 330 335	1063
CAG GTT GAT TGG AAG TCA ATG GAC CTA AGT TAC CTT TTG GAG GAC AAC Gln Val Asp Trp Lys Ser Met Asp Leu Ser Tyr Leu Leu Glu Asp Asn 340 345 350	1111
TAT GTG AAA CAC TTT GGC GAC TTG GTT AAA AAG GCT AAG CCC ATC CAC Tyr Val Lys His Phe Gly Asp Leu Val Lys Lys Ala Lys Pro Ile His 355 360 365	1159
GGA GCT GAT GCT GTT TTG AAA GCA TTT AAC ATA GAT GGT GAT GTG CGT Gly Ala Asp Ala Val Leu Lys Ala Phe Asn Ile Asp Gly Asp Val Arg 370 375 380 385	1207
ATT CAG TAC AGA GAC CAA CTA GAC TTT GAA GAT ATC GCT CGA CAG TTT Ile Gln Tyr Arg Asp Gln Leu Asp Phe Glu Asp Ile Ala Arg Gln Phe 390 395 400	1255
GGC ATT TTT GAA GAA TGG AAG GAT GGT GTA CCA CGG GCA GCA TAT AAA Gly Ile Phe Glu Glu Trp Lys Asp Gly Val Pro Arg Ala Ala Tyr Lys 405 410 415	1303
GGG ATA GTA GTT TTC CGG TTT CAA ACA TCT AGA CGT GTG TTC CTT GTT Gly Ile Val Val Phe Arg Phe Gln Thr Ser Arg Arg Val Phe Leu Val 420 425 430	1351
TCC CCT GAT TCT CTT CGA CAA CTT GGA GTT GAA GAT ACT TAG Ser Pro Asp Ser Leu Arg Gln Leu Gly Val Glu Asp Thr End 435 440 445	1393
CGAAGATATG ATTGGAGCCT GAGCAACAAT TTAGACTTAT TTGGTAGGAT ACATTTGAAA	1453
GAGCTGACAC GAAAAGTATG ACTACCACTA GCTACATGCA ACATTTTAAT GTTAATGGAA	1513
GGAACCCACT GCTTATTGTT GGAATGGATG AATCATCACC ACATCCTATT ATTCAAGTTT	1573
ACAAACATAA AGAGGAAATG TTGCCCTATA AAAACAAATT TTTTGTTTCT AAGAAGGAAC	1633
GTTACGATTA TGAGCAACTT TGGCGGCCGC GAATTC	1669

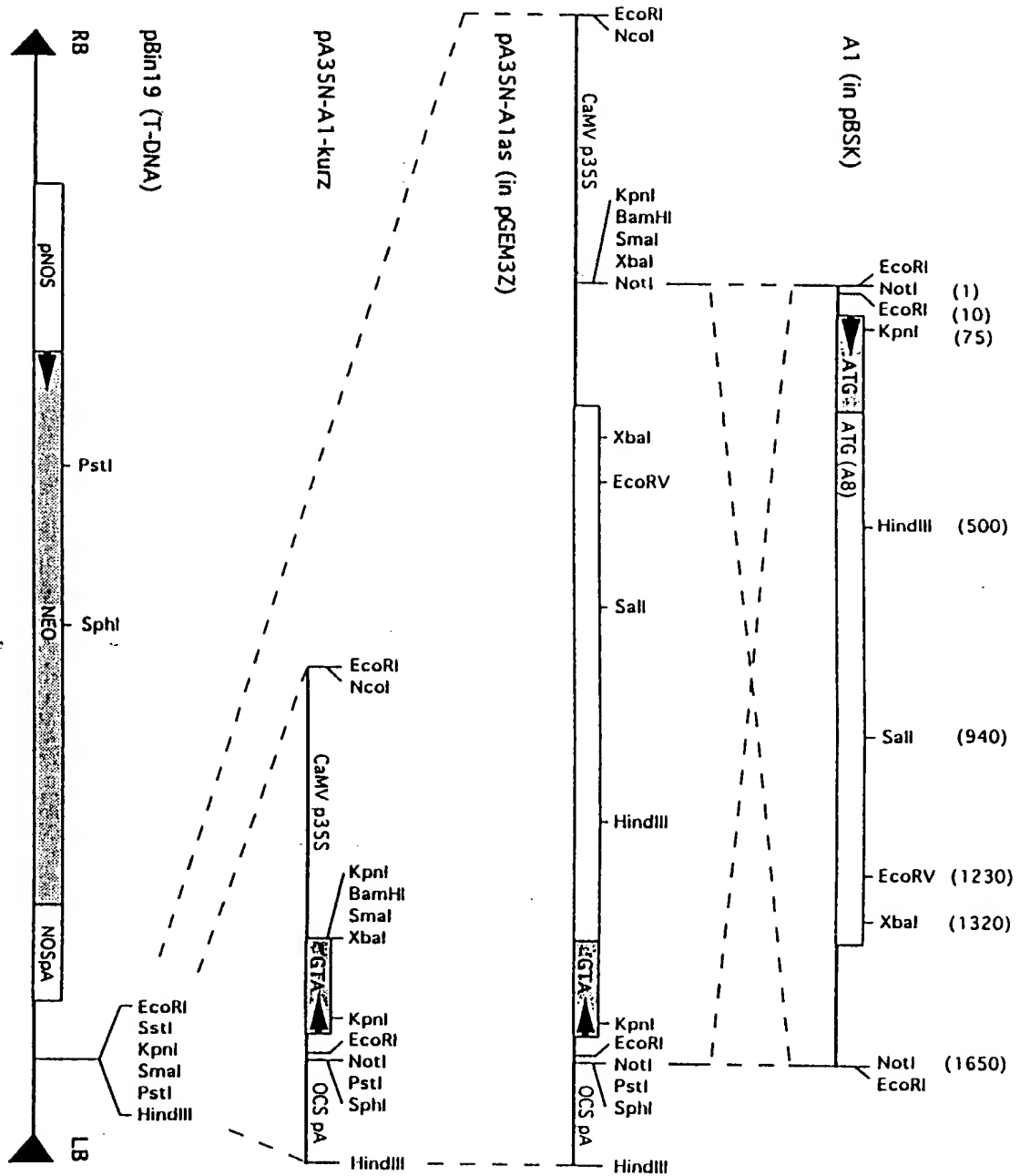
Figure 3A

Hu	Ra	Mo	Ce	St
35 (59)	36 (57)	35 (59)	33 (57)	
	92 (95)	91 (94)	38 (57)	Hu
		90 (93)	38 (57)	Ra
			38 (58)	Mo

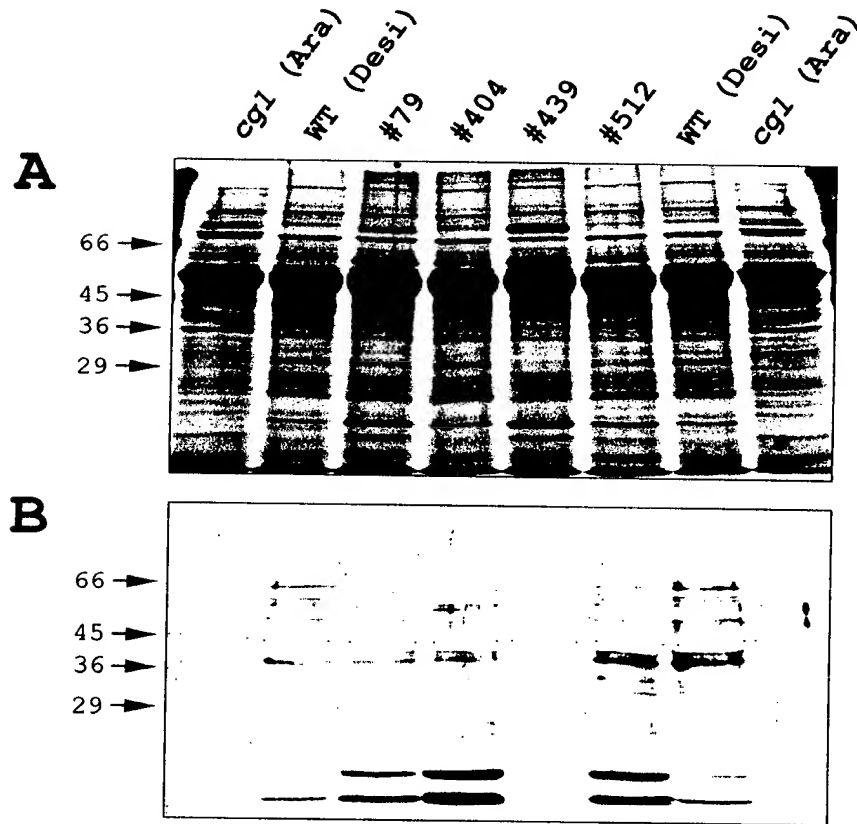
Figure 3B

A_Stb-A1	1	MRGNKFCF	DLRYLL	AA	AFIYIOMRLFATQSEY	DRLA	AAIEAENHCT
B_Ntb-A9	1	MRGNKFC	DLRYLL	AA	AFIYIOMRLFATQSEY	ADRL	AAIEAENHCT
C_Atb-Full	1	..MA	ISCDLR	LLIE	AAFMFIYIOMRLF	QTO	SADRLAAIEAENHCT
A_Stb-A1	51	SQTRLLID	KIS	QOGR	IVALEEOMK	QDOEC	ROLRALVQDLESKGIKKLI
B_Ntb-A9	51	SQTRLLID	KIS	QOGR	IVALEEOMK	QDOEC	ROLRALVQDLESKGIKKLI
C_Atb-Full	49	SOMRGLID	KIS	QOGR	IVALEEOMK	QDOEC	ROLRALVQDLESKGIKKLI
A_Stb-A1	101	GIVOMPVA	AAVVVMAC	SR	DYLERTIKSILKYOTS	VASKYPLF	ISODGSENP
B_Ntb-A9	101	GIVOMPVA	AAVVVMAC	NRADYLE	TIKSILKYOTS	VASKYPLF	ISODGSENP
C_Atb-Full	99	QGGOMPVA	AAVVVMAC	SRADYLERT	TIKSILKYOTS	VASKYPLF	ISODGSENP
A_Stb-A1	151	DVRKLALSY	GOLTYMOHLD	EPVH	TERPGEL	AYYK	IARHYKWALDQLFH
B_Ntb-A9	151	DVRKLALSY	GOLTYMOHLD	EPVH	TERPGEL	AYYK	IARHYKWALDQLFH
C_Atb-Full	149	AVTSKLSY	GOLTYMOHLD	EPVH	TERPGEL	AYYK	IARHYKWALDQLFH
A_Stb-A1	201	KHNFSRVI	ILEDDEMEIA	ADFFDY	FEAGATLLDRDKS	SIMAISSW	NDNGOMQ
B_Ntb-A9	201	KHNFSRVI	ILEDDEMEIA	ADFFDY	FEAGATLLDRDKS	SIMAISSW	NDNGOMQ
C_Atb-Full	199	KHNFSRVI	ILEDDEMEIA	ADFFDY	FEAGATLLDRDKS	SIMAISSW	NDNGOMQ
A_Stb-A1	251	FVQDD	DALYRS	DDFFPGLGWML	SKSTW	SELS	PKWPKAYWDDWLRLENHRC
B_Ntb-A9	251	FVQDD	DALYRS	DDFFPGLGWML	SKSTW	SELS	PKWPKAYWDDWLRLENHRC
C_Atb-Full	249	FVQDD	DALYRS	DDFFPGLGWML	SKSTW	SELS	PKWPKAYWDDWLRLENHRC
A_Stb-A1	301	ROFIRPE	VCRTYNFGEHG	SSLG	OFFKOYLEPIK	LNDVQVDWKS	SMDLSYLL
B_Ntb-A9	301	ROFIRPE	VCRTYNFGEHG	SSLG	OFFKOYLEPIK	LNDVQVDWKS	SMDLSYLL
C_Atb-Full	299	ROFIRPE	VCRTYNFGEHG	SSLG	OFFKOYLEPIK	LNDVQVDWKS	SMDLSYLL
A_Stb-A1	351	EDNYVKH	EGDLVKKAKPI	HGADAVLKAF	NIDGDVRIQYRD	QDQDFE	NIARO
B_Ntb-A9	351	EDNYVKH	EGDLVKKAKPI	HGADAVLKAF	NIDGDVRIQYRD	QDQDFE	NIARO
C_Atb-Full	349	EGNYTKY	ESGLV	QAPPIQ	GSDDLVLKAQNI	KDDRI	RYKDOYFEIARQ
A_Stb-A1	401	EGIFE	EWKDGV	PRAAYK	GIVVFR	QTSRRV	FLVSPDSLROLG
B_Ntb-A9	401	EGIFE	EWKDGV	PRAAYK	GIVVFR	QTSRRV	FLVSPDSLROLG
C_Atb-Full	399	EGIFE	EWKDGV	PRAAYK	GIVVFR	QTSRRV	FLVSPDSLROLG

Figur 4



Figur 5



Figur 6

